

Steven M. Ruben  
Appl. No. 10/662,429

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FROM: C. Harrow Total Pages Including Transmittal Sheet 7

COMMENTS: Bol this is the packet for AIM-I (previously  
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re add'l figures available? see last 2 pgs of transmission -  
can be taken tomorrow? same for TIF S & E i.e. today/or  
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Ruben EXHIBIT #51

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(201) 994-1700  
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FROM: C. Harrow

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COMMENTS: Bol- this is the packet for AIM-I (previously  
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re add'l figures available? see last 2 pgs of transmittal -  
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CARELLA BYRNE

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 6 Becker Farm Road  
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 (201) 994-1700  
 (201) 994-1744 (FAX)

DATE: March 14, 1996

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301,309-8512

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FROM: C. Hermans

Total Pages Including Transmittal Sheet 71

COMMENTS: Bol - this is the setup for AIM-I (provisional)  
"Fall 1996" - there are 1 or 2 questions for Steve Rubin that incl.  
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GH

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 CECCHI, STEWART & OLSTEIN  
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 CO1) 994-1700  
 CO1) 994-1744 (FAX)  
 DATE: March 14 1996

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 EXT. NO.: 525  
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<u>Bol-Benson</u>	<u>HQS</u>	<u>(301) 309-8572</u>
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FROM: S. Harned Total Pages Including Transmittal Sheet 71

COMMENTS: Bol - this is the page for AIM-I (procedures  
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*GH*

Figure 1

## Nucleotide and Amino Acid Sequence of AEM-I

-51	GGCAGGAGGGGTGGCTGGCTGACTTACAGGAGTCAGACTCTGACAGGTTTATGGCTATG	8
-16	CCGTGCTCGGCGACGGACCGACTGAATGTCGTGAGTCTGAGACTGTCCAGTACCGATAC	3
	M A M	
9	ATGGAGTCCAGGGGGACCEAGCCTGGGACAGACCTGGTGGTGTGATCGTATCTTCACA	63
4	TACCTCCAGTCCCCCTGGGTGGACCTGTCTGGACCGACGACTAGCACTAGAAGTGT	23
	M E V Q G G P S L G Q T C V L I Y I F T	
69	GTGCTCTGCAGTCTCTGTGTGGCTGTAACCTACGTTGACTTACCAACGAGGTGAAG	123
24	CACGAGGACGTGAGAGAGACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTC	43
	V L L Q S L C V A V T Y Y Y F T N E L K	
129	CAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTCTTTAAAGAAGATGACAGT	183
44	GTCTACGTCTGTTCATGAGGTTTTACCGTAACGAAACAAGAAATTTCTTCTACTGTCA	63
	Q M Q D K Y S K S G I A C F L K E D D S	
189	TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCTGCTGGCAAGTCAAGTGGCAA	248
64	ATAACCTGGGGTACTGCTTCTCTCATACTTGTGGGGACGACCGTTTCAAGTTCACCGTT	83
	Y N D P N D E E S M N S P C N Q V K N Q	
249	CTCCGTGAGTCTGTTAGAAAGATCATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT	308
84	GAGGCACTCGAGCAATCTTTCTACTAAACTCTTGGAGACTCTTTGGTAAAGATGTCAA	103
	L R Q L V R K M I L R T S E E T I S T V	
309	CAAGAAAAGCAAAAATATTTCTCCCTAGTGAGAGAAAGAGGTCTCAGAGAGTAGCA	368
104	GTCTTTTCGTTGTTTTATAAGAGGGGATCACTCTCTTCTCCAGGAGTCTCTCATCGT	123
	Q E K Q Q N I S P L V R E R G P Q R V A	
369	GCTCATAACTGGGACCGAGGAAAGCAAGCAACATGCTTCTCCAAACTCCAAGAAT	423
124	CGAGTGATGACCTGGTCTCTTCTTCTGTTGTAAACAGAGAGGTTGAGGTTCCTTA	143
	A H I T G T R G R S N T L S S P N S K N	
429	GAAAAGGCTCTGGGCGCAAAATAAACTCTGGGAATCATCAAGGAGTGGGCATTCTTC	488
144	CTTTCCGAGACCGGGGTTTTATTTGAGGACCTTAGTAGTTCCTCACCCTGAAGTAAG	163
	E K A L G R K I N S N E S S R S G H S F	
	CTGAGCACTTGCACCTGAGGAAATGGTGAAGTGGTCATCCATGAAAAAGGGTTTTACTAC	

Figure 1 (con'd)

489	-----	548
164	GACTCGTTGAACGTGAACCTCCTTACCACCTTGACCAGTAGGTACTTTTCCCAAAATGATG L S M L H L R N G E L V I H E K G F Y Y	583
549	-----	608
184	ATCTATTCCCAACATACCTTTTGGATTTGAGGAGGAAATAAAAGAAAACACAAAGAAGCAG TAGATAAGGTTTGTATGAAAGCTAAAGTCCTCTCTTATTTTCTTTGTGTTTCTTGTG I Y S Q T Y F R F Q E E I K E N T K N D	203
629	-----	668
204	AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCTATATTGTTGATG TTTGTTTACCAGTTATATAAATGTTTATGTGTTCAATAGGACTGGGATATAACAACCTAC K Q M V Q Y I Y K Y T S Y P O P I L L M	223
669	-----	728
224	AAAAGTGTAGAAATAGTTGTTGGTCTAAAGATGCAGAAATGGACTCTATTCCATCTAT TTTTCAGGATCTTATCAACAACCCAGATTTCTACGTCTTATACCTGAGATAAGGTAGATA K S A R M S C W S K D A E Y G L Y S I Y	243
729	-----	788
244	CAAGGGGAATATTGAGCTTAAGGAAAATGACAGAAATTTTGTGTTCTGTAACAAATGAG GTTCCTCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC Q G G I F E L K E N D R I F V S V T N E	253
789	-----	848
264	CACCTGATAGACATGACCATGAAGCCAGTTTTCGGGGCTTTTATGTTGGCTAACTG GTGACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGAAAAATCAACCGATTGAC H L I D M D H E A S F F G A F L V G	863
849	-----	908
	ACCTGGAAAGAAAAGCAATAACCTCAAAGTGACTATTGAGTTTCAGGATGATACCTA TGGACCTTCTTTTCTGTTATTGGAGTTTCACTGATAAGTCAAAAGTCTACTATGTGAT	
909	-----	968
	TGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAC ACTTCTACAAAGTTTCTAGACTGGTCTTGTGTTGTTGTTCTTTGTTCTTTGTTTCTTTG	
969	-----	1028
	CTCTATGCAATCTGAGTAGAGCAGCCACAACCAAAAAATCTACAACACACACTGTTCTG GAGATACGTTAGACTCATCTCTCGGTGTTGTTTTTAAAGATGTTGTGTGTGACAAGAC	
1029	-----	1088
	AAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGATCTTTCAGGACTCTACCT TTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTTCTAGAAAGTCTGAGATGGA	
1089	-----	1148
	CATATCAGTTTGTAGCAGAAATCTAGAAGACTGTGAGCTTCCAACATTAAATGCAATGG GTATAGTCAACGATCTCTTTAGATCTCTGACAGTCAAGGTTTGTAAATTACGTTACC	

Figure 1 (con'd)

1149 TTAACATCTTCTGCTTTATAATCTACTCCTTGTAAAGACTGTAGAAGAAAGCGCAACA  
 1208 AATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTCCGCTTGT  
 1209 TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCCTCCAGGTTTCCCTAAGGGACAACATC  
 1268 AGGTAGAGAGTTCATCAGATGTATCATCATCGGAGGTCCAGGAATTCCCTGTTGTAG  
 1269 CTTAAGTCAAAAGAGAGAGAGGCAACCACTAAAAGATCCAGTTTGCTGGTGCAAGTGGC  
 1328 GAATTCAGTTTTCTCTCTTCTCCGTGTTGATTTCTAGCGTCAAACGGACCACGTACCG  
 1329 TCACACCTGTAATCCCAACATTTGGGAACCAAGTGGGTAGATCAGGAGATCAAGAGA  
 1388 AGTGTGGACATTAGGGTTGTAAAACCTTGGGTTCCACCCATCTAGTGCTCTAGTTCTCT  
 1389 TCAAGACCATAGTGACCAACATAGTGAACCCCATCTCTACTGAAAGTGCAAAAATTAGC  
 1448 AGTTCTGGTATCACTGGTTGTATCACTTTGGGTTAGAGATCACTTCACGTTTTTAATCG  
 1449 TGGGTGTGTTGGACATGCCTGTAGTCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCG  
 1508 ACCCACAACCGTGTACGGACATCAGGTCGATGAACCTCTCCGACTCCGTCTCTTAGC  
 1509 TTTGAACCCGGGAGGAGAGGTTGCAGTGTGTTGAGATCATGCCACTACACTCCAGCCTG  
 1568 AAACCTGGGCCCTCCGTCTCAACGTCACACCACTCTAGTACGGTGATGTGAGGTCCGAC  
 1569 GCGACAGCGGAGACTTGTTTTC 1591  
 CGCTGTCTCGCTCTGAACCAAAG

Figure 2

Alignment of AIM-I to Human Fas Ligand  
(Similarity = 48.594 % Identity = 22.892 %)

```

4 MEVQGGPSLGQTCLVIVFVL.....LQSLCVAVTV 36
  :: ::::::::::::::: I :::::::::::::::
15 VSSASSPWAPPSTVLCPSTVPRTPGQRTPPPPPPPPPPPPPPPPP 64
37 YFTNELKQCDKYSKSGACFLKEDSYNDPNDDEESHNSPCNQVKQLRQ 86
  :: I::: ::::: I::: ::::: I::: I:::
65 PLP..LPPLKRGHNSGLCLLV...FFAVLVAVLGIGLGMFQL.FHLAK 109
87 LVKQCELRTSEETSTVQEKQDNISPLVRERGPRVAAHETGTRGRSNTL 136
  :: ::::: I::: ::::: I::: I::: I:::
110 ELAELPSTSQMNTASSLEKQIGHSPPPPEKKELRKVAHLT...GKSNR 156
137 SSPNSKNEKALGRICNSWESSRSGHSFLSNLHLRNGELVHEKGFYYEYS 186
  I I ::::: I ::::: I::: I::: I::: I:::
157 SAPLEWEDTY.....GIVLSGVKYKKGGIVINETGLYFVYS 193
187 QTYFRFQEEIKENTKNDKQWQYIYKYTS.YPDPIILMKSAHNSCNSKDA 235
  ::::: ::::: I::: ::::: I::: I::: I::: I:::
194 KVYFR.....GQSCNNIPLSHKVYMRNSKYPQDIVMEGICMSYCTTGQ 237
236 EYGLYSIYQGGEFELKENDREFVSVTNEHLIDNDHEASFFGAFLV 280
  :: I I I::: I::: I::: I::: I::: I::: I:::
238 MWR..SSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFGLYKI 281

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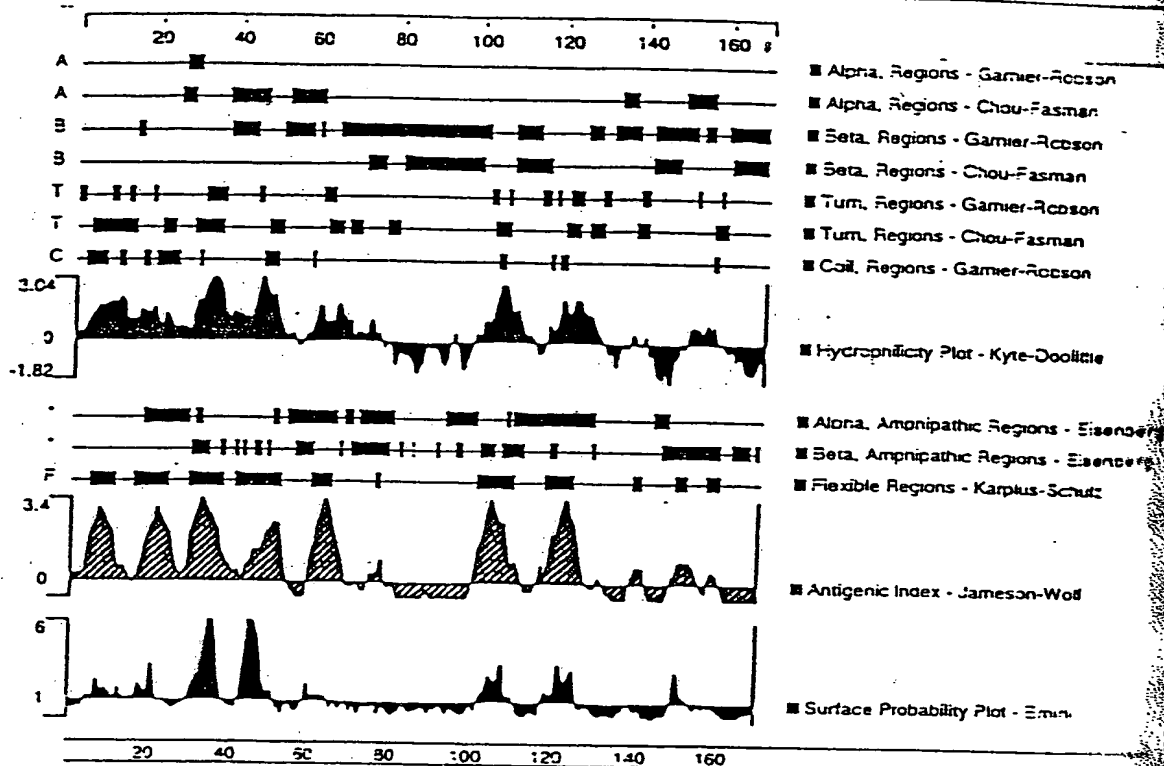


Figure 1 (con'd)

1249	TTAAATCTCTCTCTTTATAATCTACTCTCTGTAAAGACTGTAGAAGAAAGCGCAACAA	1208
	AAATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTCTCTCGCTTGT	
1209	TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCTCCAGGTTTCTTAAGGGACAACATC	1268
	AGGTAGAGAGTTCATCACATAGTGTCTCATCTCGGAGGTCCAAAGGAATTCCTGTTGTAG	
1269	CTTAAGTCAAAAGAGAGAAGAGGACCACTAAAAGATCGCAGTTTGCCTGGTGCACTGGC	1328
	GAATTCAGTTTTCTCTCTCTCGTGGTGATTTTCTAGCGTCAAACGGACCACGTACCG	
1329	TCACACCTGTAATCCCAACATTTGGGAACCAAGTGGGTAGATCAGGATCAAGAGA	1388
	AGTGTGGACATTAGGTTTGTAAAACCTTGGGTCCACCCATCTAGTGCTCTAGTTCTCT	
1389	TCAGACCATAGTGACCAACATAGTGAAACCCCATCTCTACTGAAAGTGCAAAAATTAGC	1448
	AGTTCTGGTATCACTGGTTGTATCACTTGGGGTAGAGATGACTTCACGTTTTTAATCG	
1449	TGGGTGTGTTGGCACATGCTGTAGTCCAGCTACTTGAGAGGCTGAGGCAGGAGAATCG	1508
	ACCCACACAACCGTGTACGGACATCAGGTCGATGAATCTCCGACTCCGTCTCTTAGC	
1509	TTTGAACCCGGGAGGCAGAGTTGCAGTGTGGTGAGATCATGCCACTACACTCCAGCCTG	1568
	AAACTTGGGCCCTCCGTCTCCAACGTCAACCACTCTAGTACGGTGATGTGAGGTCCGAC	
1569	GCGACAGAGCGAGACTTGGTTTC	1591
	CGCTGTCTCGCTCTGAACCAAAG	

Denotation: Shade (with solid black) residues that match *Delipia* exactly.

Thanks  
Charlie



Steve

do you have such a  
 Fig for AIM-1 (Foligant)?

if so please fax to me

Thanks

Charlie

Alignment Report of Unrooted 1 Clustal method with PAM50 residue weight 200.  
 Thursday, March 14, 2006 11:10 AM

Page 1

	10	20	30		
1	M A M M E V Q G G P S	- - - - - G Q C V L - V - F T V L	ACT 1		
1	M Q C P M N Y P C P C	- - - - - N V D S S A L S S W A P D G S V	FAS LIGAND	U06948.pep	
1	M - - - - - - - - - -	- - - - - - - - - -	U06948.pep		
1	M - - - - - - - - - -	- - - - - - - - - -	U06948.pep		
	40	50	60		
26	U Q S L E V A V T Y V Y	P N E L K Q N G Q K Y S K S G L A	ACT 1		
31	P C P S L P P R G - - -	P D Q R R P P P P P P P P V S I P L P	FAS LIGAND	U06948.pep	
2	- - - - - - - - - -	- - - - - S S S M T R D V E	U06948.pep		
9	L P R V L G - - - - -	- - - - - - - - - -	U06948.pep		
	70	80	90		
56	C F L K E D D S Y W D P N D E E S M I N S S C W I Q V K W Q L R	ACT 1			
57	- - P P S Q P L P L P P L T P L K K K D M T N L W L P V V	FAS LIGAND	U06948.pep		
12	- - L A E A L - - - - -	- - - - - K K - G G P Q G S R R C L	U06948.pep		
17	- - - - - - - - - -	- - - - - - - - - -	U06948.pep		
	100	110	120		
86	P L V R K M - R S S E - - - - - V E K C I G N S P L V R	ACT 1			
85	- - - V L V A L V G M I G - N Y Q L F H L K E L A S C L S	FAS LIGAND	U06948.pep		
32	- - S I F S F L - V A I G A L - L S C L - - - - - G V G F G R E	U06948.pep			
21	L L C L L V - - - - -	- - - - - - - - - -	U06948.pep		
	130	140	150		
126	E E P Q R V A A H - T G T R G R S N L L S S P N S K N S E K	ACT 1			
124	E F T - N G C L K V S S E K Q L A N B S I T P S I E K L S E P L R	FAS LIGAND	U06948.pep		
62	E S P K D L S L - S P L A Q A V I S S K L Y S D - - - - - K	U06948.pep			
34	C L P - G V I G L P S I A D T A R Q R P K N H L A H S T L K	U06948.pep			
	160	170	180		
146	A L G R K - N S - - - - - - - - - - V E S S E S C H S F L S I N	ACT 1			
143	S V A H L T G N P H I S R S I P L E W E D T Y C T A L - S G	FAS LIGAND	U06948.pep		
88	P V A H L V A N P Q A E G O - L Q W L N R R I A N I A L L A N G	U06948.pep			
6	D A A H L - - - - - - - - - - S K Q N S L L W R A N T D R A L F L Q D I G	U06948.pep			
	190	200	210		
167	L N L A N M E L V - H E K G P Y Y Y Y S D E Y F R F Q E E	ACT 1			
172	V K Y K K G L V - M E - - - - - G L Y F V Y S K V Y F R G Q S I C N	FAS LIGAND	U06948.pep		
177	V E L R D N O L V V S E G - Y L - - - - - Y S G V L F K G Q G L	U06948.pep			
92	Y C L S I N I N S L L V - - - - - - - - - - Y V Y C V I V E S L K A Y S	U06948.pep			
	220	230	240		
157	K E N - K M D K G I V I Q I Y - Y K Y - - - - - Y P D P L - - - - - M K S I	ACT 1			
202	N Q P - - - - - - - - - - L N R K V Y N R N I S K Y D E D - V L M E E	FAS LIGAND	U06948.pep		
146	- - - - - P S - E V - - - - - - - - - - M C L S R - A V S Y - - - - - K V I N L - S A	U06948.pep			
177	P K A L P S S P L Y L A H E L C L - - - - - S Q Y P F K V P L - - - - - S S I	U06948.pep			



HGS

# Facsimile Cover Sheet

Human Genome Sciences, Inc.  
9620 Medical Center Drive, #300  
Rockville, MD 20850-3338  
(301) 309-8504 (301) 340-7159 Fax



DATE: 3-14-96

TO: Charles Herron

FAX #: 201-994-1744

FROM: Steve Ruben

## COMMENTS:

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Number of Pages (including cover): 4

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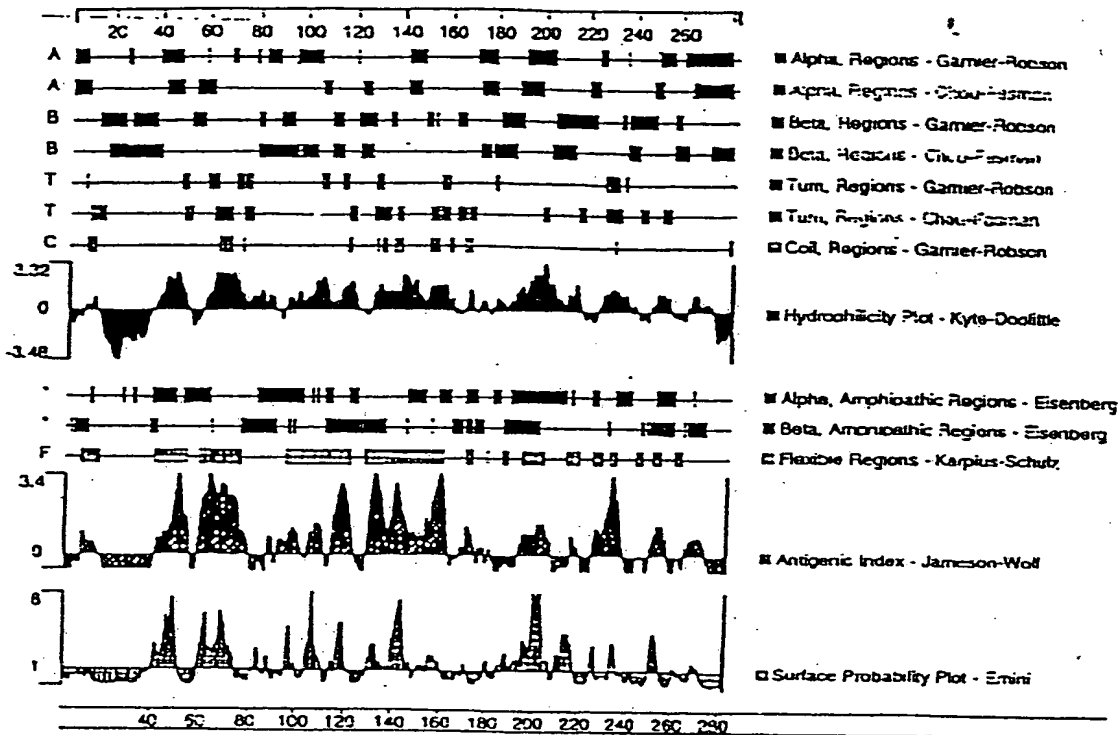
RUS-

201001/11/1/3/7

Page 1

Alignment Report of Unlabeled, using Clustal method with PAM250 residue weight table.  
Thursday, March 14, 1996 11:16 AM

	10	20	30		
1	M A M M E V Q G G P S	- - - - - G Q	C V L I V T T V L	AIM 1	
1	M Q Q P M N Y P C P Q	- - - - - W V D S S A	S S W A P D G S V	FAS LIGAND	U06948.pep
1	M	- - - - -	- - - - - T P P E R L	unfa.pep	
1	M	- - - - -	- - - - -	unfb.pep	
	40	50	60		
26	L Q S L C I V A V T Y V Y P T N E L K Q H Q C K Y S K S I G I A	AIM 2			
31	P C P S C G P R G	- - - - - P Q R R P P P P P P V S P L P	FAS LIGAND	U06948.pep	
2	- - - - -	- - - - - S T E S M I R D V E	unfa.pep		
9	L P R V C G T T	- - - - -	- - - - -	unfb.pep	
	70	80	90		
56	C F L K L D C S Y W D P N E E S M N S P C W Q V K W Q L R	AIM 1			
57	- - - - - P P S Q P L P L P L T R L K K K D H N T N L W L P V V	FAS LIGAND	U06948.pep		
12	- - - - - L A E A L P	- - - - - K K T G G P Q G S R R C L	unfa.pep		
17	- - - - -	- - - - - T W L I	unfb.pep		
	100	110	120		
86	Q L V R K M	- - - - - R T S E E L - - - - - S V Q E K Q Q N S P L V R	AIM 1		
95	F E M V L V A	- - - - - V G M G L G - - - - - M Y Q L F H L O K E A E L R	FAS LIGAND	U06948.pep	
32	P S L E S E L	- - - - - I V A I G A T L Y C L L M F G V G P Q R E	unfa.pep		
21	L L G L L V	- - - - -	- - - - - L P C A Q	unfb.pep	
	130	140	150		
116	Z R G F Q R V A A E T T G T R G R S N T L S I S P N S K N S K	AIM 1			
114	E P T - N Q S L K V S S F E K Q T A N D S T P S E K K E P R	FAS LIGAND	U06948.pep		
62	E S P R D L S L - - - - - S P L A Q A V K S S S K T S S D - - - - - K	unfa.pep			
34	C L P - C V I G - - - - - P S A A O T A I R Q L P K M H L A H S T L K	unfb.pep			
	160	170	180		
146	A L G I R K E N S I - - - - - W E S S S S G H S F L S I N	AIM 1			
143	S V A H L T G N P E S I R S I P L E W E D T Y G T A L I - S G	FAS LIGAND	U06948.pep		
88	S V A H V I V A N P Q A E G Q - L Q W L N R R I A N A L L A N G	unfa.pep			
63	P A A H L T G D P - S K Q N S L L W R A N T D R A F L Q D I G	unfb.pep			
	190	200	210		
167	L H L R N G R L V I H E K G E Y Y I Y S Q I T Y F R I Q I E E -	AIM 1			
172	V K Y K K G G L V - N E T G L Y F V Y S K V Y F R G Q S C N	FAS LIGAND	U06948.pep		
117	V I E L R D N Q L V V P S E G - Y L - Y S Q V L F K G G G C -	unfa.pep			
92	F S L I S I N N S L V N T S G - Y F V Y S O V V E S C K A Y S	unfb.pep			
	220	230	240		
157	K E N T R N D K Q M V Q Y - Y K Y T S I - Y P D P L E L M K S I	AIM 1			
202	N Q P - - - - - L N H K V Y M R N S K Y P E D L V L M E E	FAS LIGAND	U06948.pep		
146	- - - - - P S T E V L L T H - - - - - S R - A V S Y Q T K V N L L S A	unfa.pep			
122	P K A P S S P - Y L A E L V C - P S S Q Y P F E V P - L S S	unfb.pep			



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